Sorting single satellite cells from individual myofibers reveals heterogeneity in cell-surface markers and myogenic capacity.

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Public Summary:
This work enables a new approach for understanding stem cell behavior at a single cell levels. Tissue stem cells live in their organ niches where they represent a minute cell population. A great deal more can be understood about the properties of these regenerative cells and their therapeutic potential using a single cell analysis (as compared to conventional bulk cell preparations).

Scientific Abstract:
Traditional cell-screening techniques such as FACS and MACS are better suited for large numbers of cells isolated from bulk tissue and cannot easily screen stem or progenitor cells from minute populations found in their physiological niches. Furthermore, these techniques rely upon irreversible antibody binding, potentially altering cell properties, including gene expression and regenerative capacity. To address these challenges, we have developed a novel, label-free stem-cell analysis and sorting platform capable of quantifying cell-surface marker expression of single functional organ stem cells directly isolated from their micro-anatomical niche. Using our unique platform, we have discovered a remarkable heterogeneity in both the regenerative capacity and expression of CXCR4, beta1-integrin, Sca-1, M-cadherin, Syndecan-4, and Notch-1 in freshly isolated muscle stem (satellite) cells residing on different, single myofibers and have identified a small population of Sca-1(+)/Myf5(+) myogenic satellite cells. Our results demonstrate the utility of our single-cell platform for uncovering and functionally characterizing stem-cell heterogeneity in the organ microniche.

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